

## AMENDMENTS TO THE SPECIFICATION

**On page 4, please replace the paragraph beginning on line 5 and ending on line 7 with the following amended paragraph:**

Figure 6 shows an alignment of human KIA1872 (SEQ ID NO:5), macaque (SEQ ID NO:6), mouse jittery (SEQ ID NO:7), human NIP2 (SEQ ID ~~NO:8~~ NO:26), and mouse NIP2 (SEQ ID ~~NO:9~~ NO:27) polypeptides.

**On page 4, please replace the paragraph beginning on line 19 and ending on line 20 with the following amended paragraph:**

Figure 13 (SEQ ID NOS:14-21) shows a sequence alignment of predicted ATCAY protein sequences with related genes across species.

**On page 4, please replace the paragraph beginning on line 25 and ending on page 5, line 3 with the following amended paragraph:**

As used herein, the term "Cayman ataxia" or "~~Cayman ataxia~~" when used in reference to a protein or nucleic acid refers to a protein or nucleic acid encoding a protein that, in some mutant forms, is correlated with ataxia. The term Cayman ataxia encompasses both proteins that are identical to wild-type Cayman ataxia and those that are derived from wild type Cayman ataxia (*e.g.*, variants of Cayman ataxia or chimeric genes constructed with portions of Cayman ataxia coding regions). In some embodiments, the "Cayman ataxia" is the wild type nucleic acid (SEQ ID NO: 3) or amino acid (SEQ ID NO:4) sequence. In other embodiments, the "Cayman ataxia" is a variant or mutant (*e.g.*, including, but not limited to, variants resulting in disease).

**On page 88, please replace the paragraphs beginning on line 22 and ending on page 89, line 8 with the following amended paragraphs:**

The KIAA1872 (identified above as the Cayman ataxia protein) protein is a protein of unknown function. According to the predicted proteins found at various genome sites, it isn't even clear what the N-terminal amino acid, i.e. start of translation, of the protein is. The sequence of macaque, mouse and human of the predicted protein, and they are highly

conserved. In contrast, the sequences of mouse and human protein just before the presumed translation start are not homologous (See below), indicating the MGTT is indeed the start of the protein.

PSSDAESAPASILFL  
LGSEGPSVSDAQLHPGRARLCLPVRRRGCLSCRGVIPASSQCLFPAPMGTTTEAT ~~(SEQ ID NO:5)~~ (SEQ ID NO:24)

ASFHQAPRLGTIEKCPPLCPSDSAEAASATEIIFWVTRVSRPLLFPALMGTTTEAT ~~(SEQ ID NO:6)~~ (SEQ ID NO:25)

The 5' sequence near this methionine has partial homology to the Kozak consensus sequence: CCAGCTCTCATGG (SEQ ID NO:22) matches 8/13 to GCCGCCACCAUGG (SEQ ID NO:23) – one of very few matches in the region of interest, and the first Methionine after an in-frame stop.

Please insert the attached Sequence Listing as new pages --109-203--.

#### **IN THE CLAIMS**

Please renumber the Claims pages from pages "110-112" to --204-206--.

#### **IN THE ABSTRACT:**

Please renumber the Abstract page from page "113" to --207--.

## **AMENDMENTS TO DRAWINGS**

Figure 15 has been amended to provide sequence identifiers. Applicants' amendments do not introduce new matter.